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FIG. 1

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FIG. 2

BpTPS1 :	MKVATLFFLASSV----CVLG-----	D P Q F V K L E A S V L R G S T Y K D S Q K G A K P F M L E K R A D D G :	53
ScTPS1 :	MKLKTVRSAVLSSLFASQVLGKIPAAANKRDDDSNSKREVKLPFEEKLYGDSLENVGSDKKPENVRLLKRADG :	70	
ScTPS2 :	MKL S V L T F F V D D A L L V C S S I V D A G V - - T D F P S L P S N E V Y V K M N F Q K K Y G S S F E N A L D T K G R T R L M T R D D :	68	
ScTPS3 :	MKLQLAAVATLAVL-TSAPAFGRVLP-----D G Y V K I P F T K K - - - - - K N G D N G E L S K R S N G :	50	

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hPypS1 : S V T M E L Q N A Q S F Y Q V E I I E I G S D K O E V G V L I D T G S S D L W V M N S N N S Y C S S S S T K K L K R -- D G P A D A L Q K G : 120
ScyP51 : Y E E I I I T N R Q S F V S V D L E V G T P P O N V T V L V D T G S S D L W I M G S D N P V C S S N S M G S S R R R V I D K R D D S S S G G : 140
ScyP52 : Y E L V E L T N Q N S F Y S V E L D P T P F O K V T V L V D T G S S D L W T V G S D N P V C S S S T K K D L T T G S S F -- K Q V N K D A L A : 136
ScyP53 : R E K F V L A N Q S F Y S V E L A I G T P S O N I V T V L L D T G S S D L W V P G K G N P V C G S -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- : 99

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hPyPS1 : T-EIISYADRTFARGTWGYDDVTFNGBTVNDLSLAVADEDTSSTGVFGIGLRELETTYSGG---GPQH Y : 255
ScyPS1 : Y-FSISYGDGTFFASGTFGTDTVLDLSDLNVTGLSFAVANETNSTMVGLIGLPELEVTYSGS-TASESGKAY X : 274
ScyPS2 : E-ESIAYGDTTFASTGQTLQDLSLNLDLNITGLSFAVANETNSTGVGLIGLPGLESTYSGVLLSDVVQKSY : 261
ScyPS3 : S-EFVAVGCDTGYLQCFCDKIKYVNDLISGCFSPAVANENSTGVGLIGLSTTYSGVVAITMDKRSV Y : 192

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HsPYS1 : IVDNLPPFKMVDQGLINRAAAYSVYLNSTESSTASILFGAVDQSKYTGSGVGLLPIINTAASYGYOKPLRLOE : 325
ScPYS1 : KYDNEFPIVLLKNSCAIKSNTYSLNDSDAMHGTILFGAVDESKYTGLTTIPIVNTLSASGFSSPIQFDV : 344
ScPYS2 : TYMMNEFPMVLLKNSGVIKSTAYSLNDSDSKEGTTILFGAVDEGKYAGDLTTIPIVNTLQHEYKDPQFDV : 331
ScPYS2 : FVMMNEFPMVLLKNSGVIKSTAYSLNDSDSKEGTTILFGAVDEGKYAGDLTTIPIVNTLQHEYKDPQFDV : 262

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HsPYS1 : TLSAINTVSDSRGQQ--AISIGSGAAAAALLDTGTTLTYAPSEIVEKLAETTGFDYSSSVGAVVARCRDV--D : 391
ScPYS1 : TINGIGISDSGSSNK--TLLTTKIPALSDSGTTLTYLPQTUVVSMIAFELGAGQYSSRIGTYVLDLCPSD--D : 410
ScPYS2 : TLOGLGLTSKGDKEKDNLTTTTLTKEVLLDGSGTTISYMPTELKVLMQAVGATYSSAYGTYVIMDCIKEMEE : 401
ScPYS2 : ...-CTDVRNNTLTITKLRNMLDGSGTTISYMPTELKVLMQAVGATYSSAYGTYVIMDCIKEMEE : 328

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HpYPS1 : SYA VNF DFG QGK VIE APL SSFL I AL QTN SGE VSS Y CAL G I P S - SG D E S F T L G D T F L R N A V E V A D L E G Y Q I A : 460
ScYPS1 : SME I V F D F G G F E D I N A P L S S F I L S T G T - - - T - - - C L G I I L P T S S D T G T I L G D S F L T N A Y V V Y D L E N L E I S : 473
ScYPS2 : E S S I H F D F G G F Y I L S N W L S D F Q L V T D S R S N T I - - - C L G I I A P S D P T - I I L G D N F L A N T Y V V Y D L D N M E I S : 466
ScYPS2 : K S S I H F D F G G F Y I L S N W L S D F Q L V T D S R S N T I - - - C L G I I A P S D P T - I I L G D N F L A N T Y V V Y D L D N M E I S : 392

```

```

H1Y1PS1 : VSSVKTSTSSGSGSTSESSSTSSSHS-----SNGPRTVGFSLCAVLCAFLISILV----- : 574
S1C1Y1PS1 : -----SGNLTTSTASATSTSS-----KRNVGDHIVPSLPLTTLISLLFA----- : 567
S1C1Y2PS2 : SKGQKTQNTSTAALSIKSSTSSSTGMLSPSSSFRKENGHHNLNPFFFARFITAIFH----- : 594
S1Y2PS2 : -----P-----T-----A-----T-----C-----S-----C-----S-----C-----L----- : 518

```

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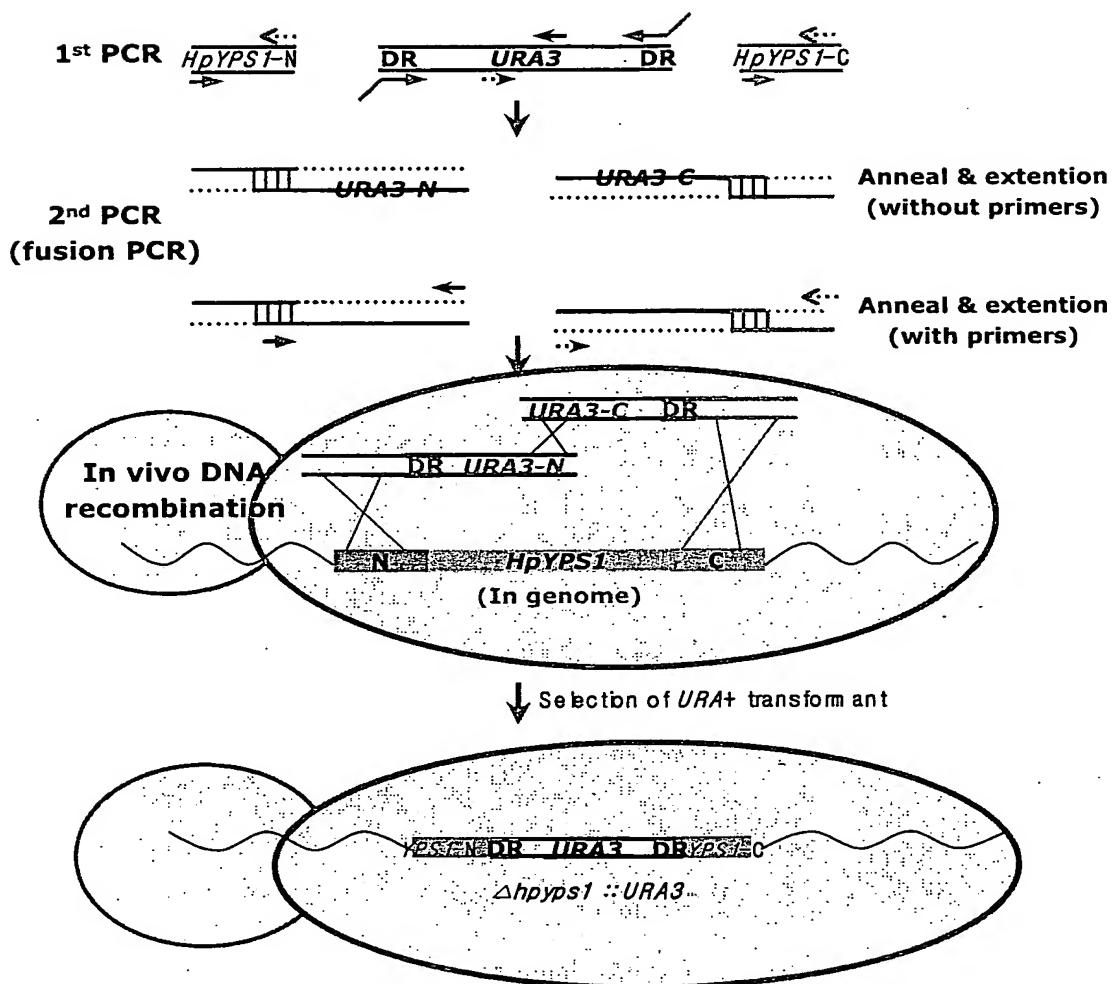
H2YPS1 : -VC- : 576
ScYPS1 : --FI : 569
ScYPS2 : --HI : 596

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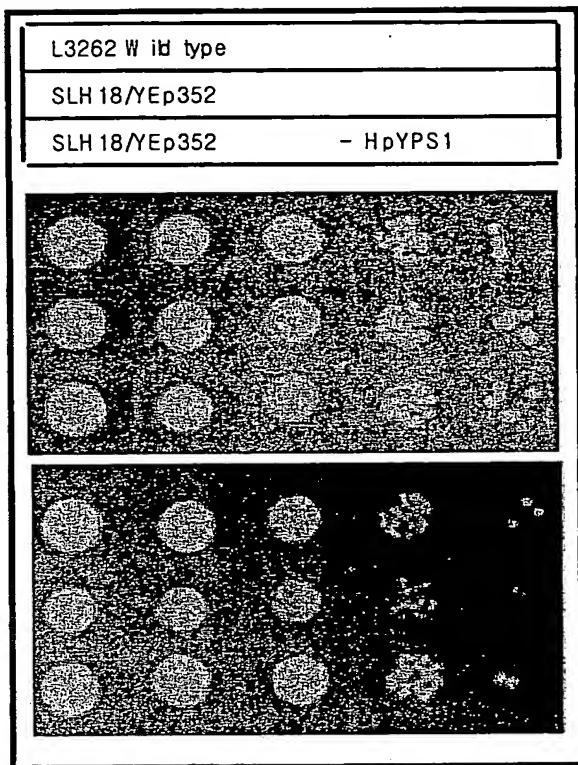
FIG. 3



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FIG. 4



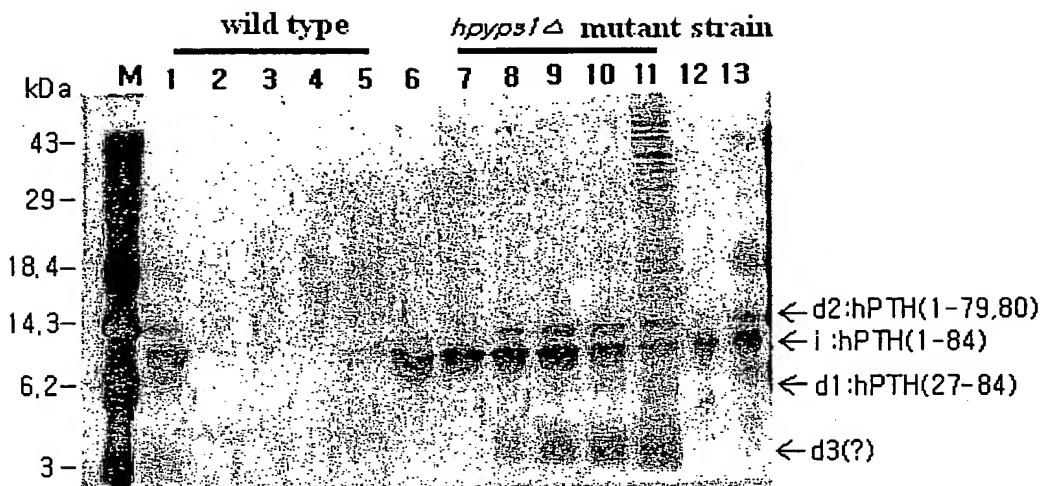
30 °C , 48 hr

37 °C , 48 hr

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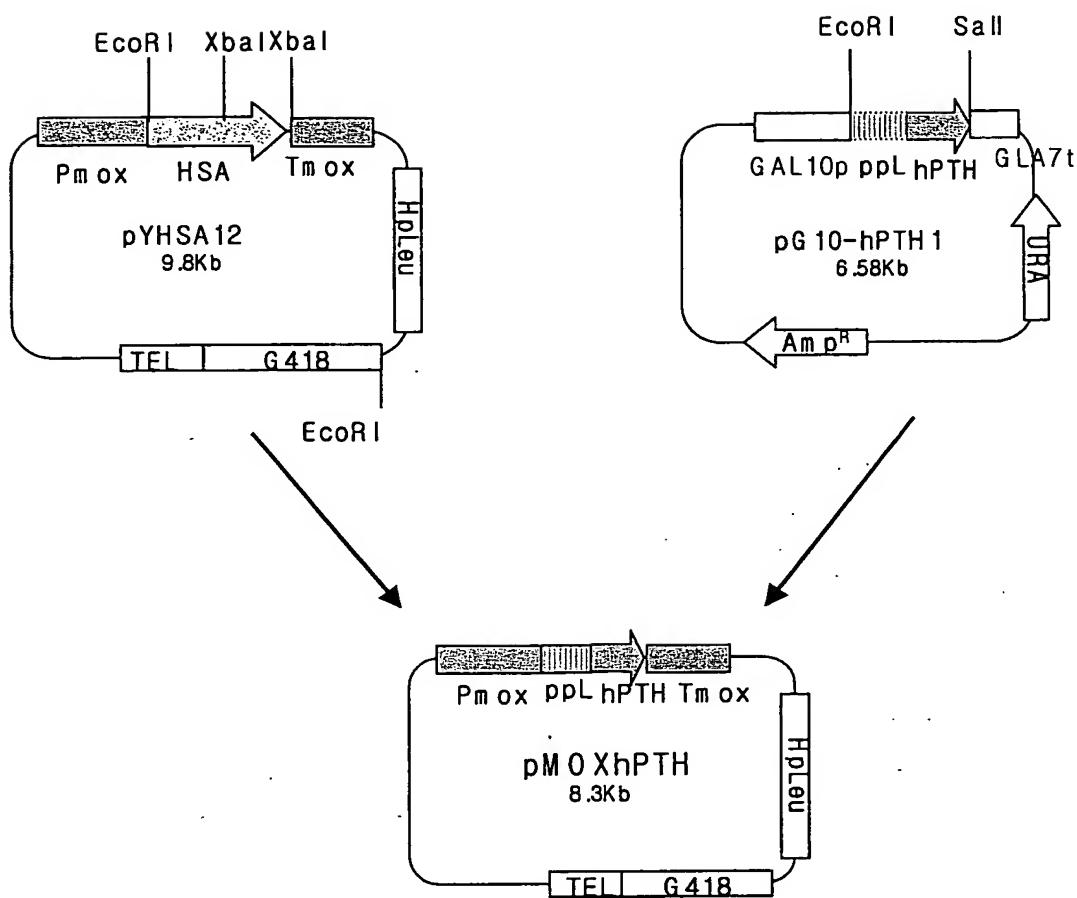
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FIG. 5

**Lane M: Molecular marker**

- 1: wild type, 0-h reaction
- 2: wild type, 2-h reaction
- 3: wild type, 4-h reaction
- 4: wild type, 6-h reaction
- 5: wild type, 24-h reaction
- 6: distilled water + hPTH, 0-h reaction
- 7: mutant strain, 0-h reaction
- 8: mutant strain, 2-h reaction
- 9: mutant strain, 4-h reaction
- 10: mutant strain, 6-h reaction
- 11: mutant strain, 24-h reaction
- 12: hPTH 100 ng
- 13: hPTH 200 ng

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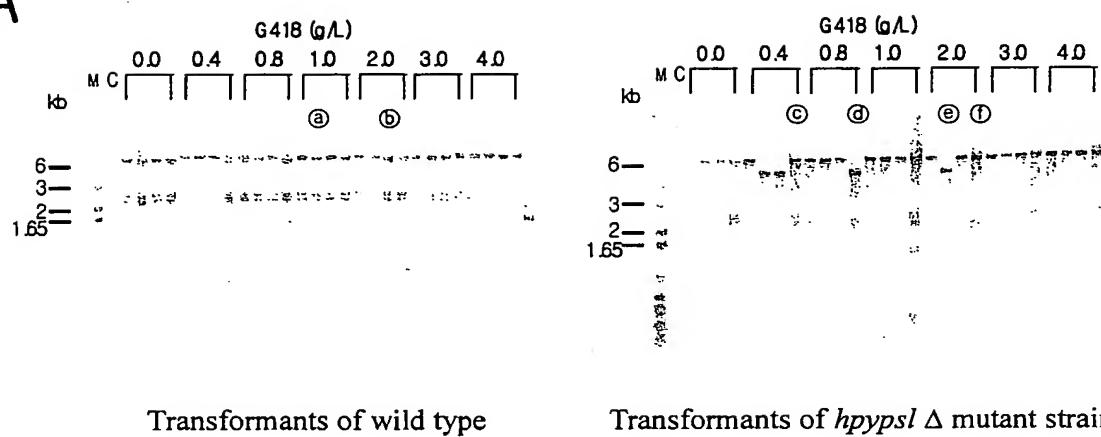
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FIG. 6

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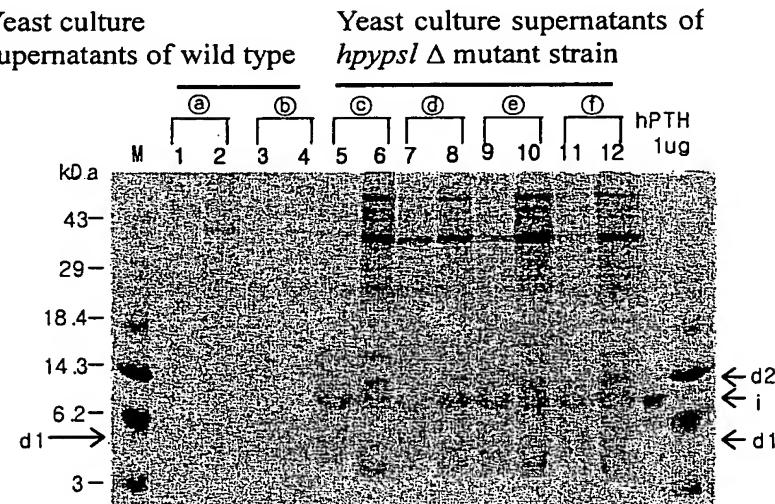
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FIG. 7

A



B

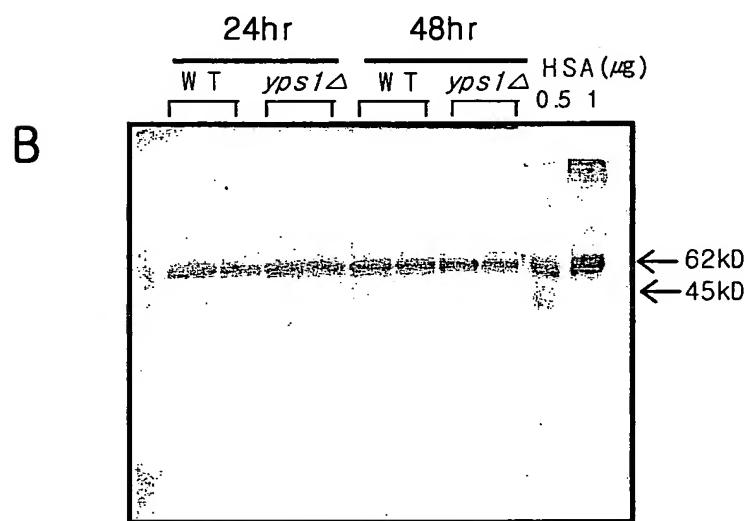
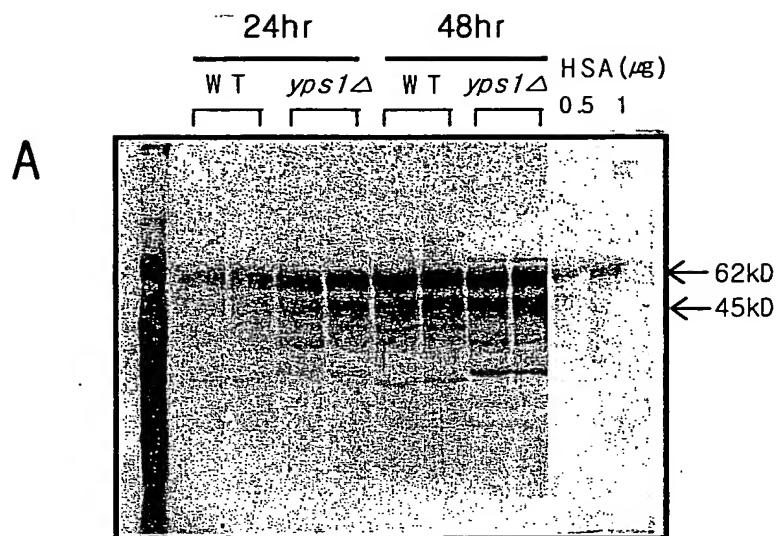


Lane 1, 3, 5, 7, 9, 11 : 12hr after initiation of the cultivation
 Lane 2, 4, 6, 8, 10, 12 : 24hr after initiation of the cultivation

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FIG. 8

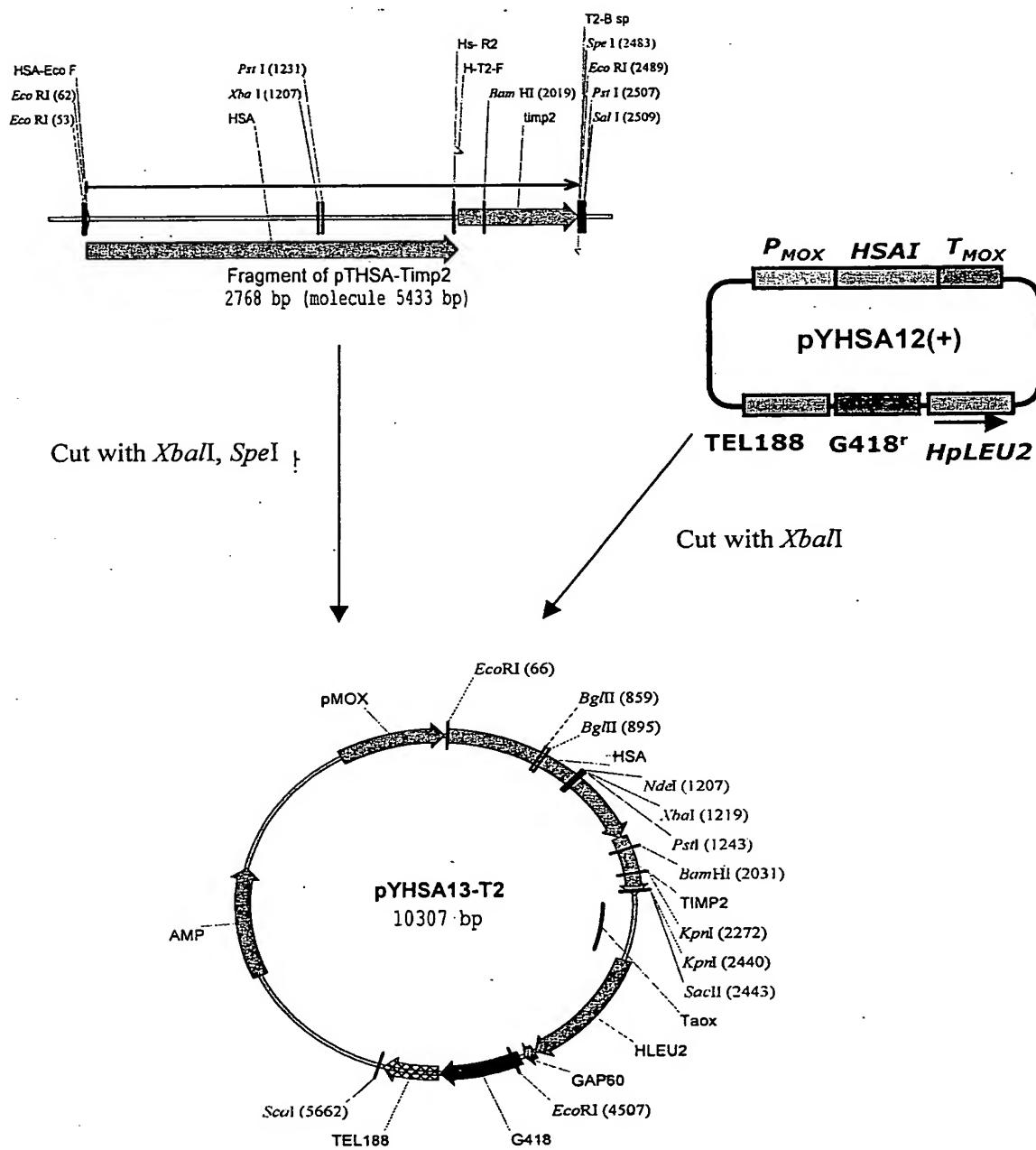


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FIG. 9

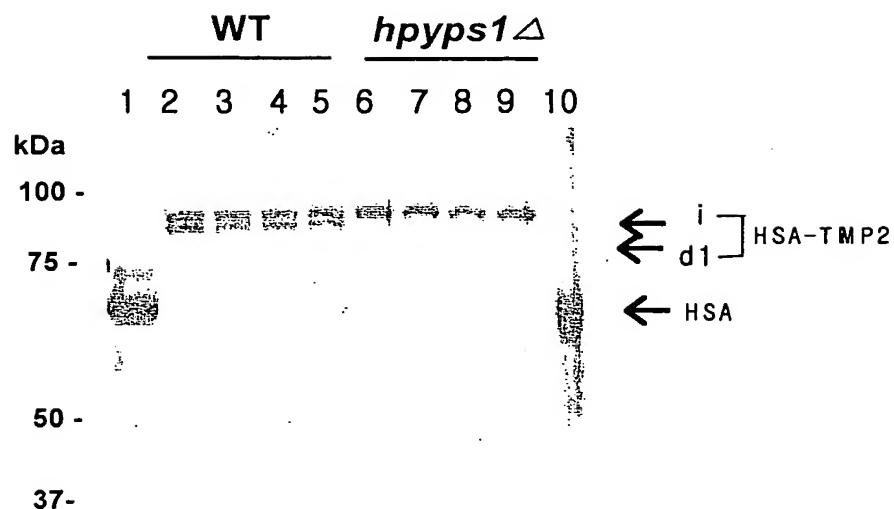
HSA-TIMP2 fusion gene



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FIG. 10



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